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UNITED STATES PATENT AND TRADEMARK OFFICE

BEFORE THE BOARD OF PATENT APPEALS AND INTERFERENCES

Ex parte JOHN B. HARLEY and JUDITH A. JAMES, Appellants¹

Appeal 2009-010657 Application 08/781,296 Technology Center 1600

Decided: May 25, 2010

Before CAROL A. SPIEGEL, DEMETRA J. MILLS, and STEPHEN WALSH, Administrative Patent Judges.

SPIEGEL, Administrative Patent Judge.

DECISION ON APPEAL

Appellants appeal under 35 U.S.C. § 134(a) from an Examiner's final rejection of claims 27 and 29. Claims 3-40, the only other pending claims, are withdrawn from consideration as directed to a nonelected invention. We have jurisdiction under 35 U.S.C. § 134. We REVERSE.

The real party in interest is the Oklahoma Medical Research Foundation, Oklahoma City, OK (Second Resubmitted Brief on Appeal, filed 12 October 2006 ("App. Br.") at 4). This decision also refers to the Examiner's Answer mailed 8 January 2007 ("Ans.") and the Reply Brief filed 1 March 2007 ("Reply Br.").

I. Statement of the Case

The subject matter on appeal is directed to peptide compositions containing Epstein-Barr viral peptides. Claim 27 is illustrative and reads (App. Br. 11, emphasis added):

A peptide composition comprising a peptide molecule consisting of about 40 amino acids or less and comprising a peptide sequence selected from the group consisting of PPPGRRP (SEQ ID NO:1), GRGRGRGG (SEO ID NO:2), RGRGREK (SEO ID NO:3). GPORRGGDNHGRGRGRGRGRGGGRPG (SEO ID NO:13), GGSGSGPRHRDGVRRPQKRP (SEO ID NO:14), GTGAGAGARGRGG (SEO ID N O:17), SGGRGRGG (SEO ID NO:18), RGGSGGRRGRGR (SEQ ID NO:19), SSSSGSPPRRPPPGR (SEQ ID NO:21), RPPPGRRPFFHPVGEADYFEYHOEG (SEO ID NO:22), GPSTGRPG (SEO ID NO: 25), GQGDGGRRK (SEQ ID NO:26), DGGRRKKGGWFGKHR (SEO ID NO:27). GKHRGOGGSN (SEO ID NO:28), GOGGSNPK (SEO ID NO:29), NPKFENIA (SEO ID NO:30), RSHVERTT (SEQ ID NO:31), VFVYGGSKT (SEO ID NO:32), GSKTSLYNL (SEO ID NO:33), CNIRVTVC (SEO ID NO:36), PPWFPPMVEG (SEQ ID NO:38) and combinations thereof, wherein the peptide is present in either free form or bound to a carrier molecule.

The Examiner rejected claims 27 and 29 under 35 U.S.C. § 112, first paragraph (lack of written descriptive support), and under 35 U.S.C. § 102(b) as anticipated by Chen² (Ans. at 3-5).

II. Written Description

According to the Examiner, while the Specification expressly discloses the individual peptides having SEQ ID NOs: 1-3, 13, 14, 17-19, 21, 22, 25-33, 36, and 38, it does not provide an adequate written description of a genus of combinations thereof or sequences larger than the peptides recited in claim 27 (Ans. at 3-4 and 7-8). It is the Examiner's position that (A) the specifically disclosed species "are not representative of the genus because the genus is highly variant" (*id.* at 4) and (B) the claimed composition is not limited to a peptide composition "consisting of" 40 amino acids or less (*id.* at 8). The Examiner argues that, absent a showing characterizing the structural and functional components of the recited peptides, the effects of changing even a single amino acid are largely unpredictable as to which ones will have a significant effect on binding (*id.* at 9). The Examiner cites Russell³ as evidence of the unpredictability of the relationship between sequence, structure, and function (*id.*).

Appellants argue that "those of skill in the art would readily understand that these recited sequences could be included within larger peptide segments (but no longer than about 40 amino acids as recited) while

^a M. Chen et al., Delineation of a 16 Amino Acid Sequence that Forms a Core DNA Recognition Motif in the Epstein-Barr Virus EBNA-1 Protein,

²⁰⁵ VIROLOGY 486-495 (1994) ("Chen").

Russell and Barton, Structural Features can be Unconserved in Proteins with Similar Folds, 244 JOURNAL OF MOLECULAR BIOLOGY 332-350 (1994) ("Russell").

still accomplishing the goals of the present invention – binding to autoantibodies" (App. Br. 6). According to Appellants, a skilled artisan would "readily understand that the recited peptides can be used in combination to identify a plurality of antibodies, each of which binding [sic] to distinct peptides" (id. 9). Appellants reiterate that claim 27, as written, properly excludes peptides of greater than 40 amino acids (Reply Br. 6-7).

Based on the positions advanced by the Examiner and Appellants, the issues relative to the written description rejection are (1) what is the scope of claim 27 and (2) does the Specification provide adequate written descriptive support for the peptide composition of claim 27, including both combinations of the recited peptides and peptides of longer than the recited peptides.

During examination of a patent application, a claim is given its broadest reasonable construction consistent with the specification. *In re Prater*, 415 F.2d 1393, 1404-05 (CCPA 1969).

Here, we agree with Appellants that claim 27, when properly construed, recites a composition containing a peptide molecule with two required limitations – it consists of about forty amino acids or less and it contains a sequence selected from the recited Markush group. Thus, claim 27 does not encompass a composition containing a peptide containing the sequence PPPGRRPGRGRGRGG, i.e., SEQ ID NO:1 joined to SEQ ID NO:2. This interpretation is consistent with original claim 8. Original claim 8 read:

 The diagnostic test of claim 6 wherein the reagents are used to detect antibodies to peptides from Epstein-Barr virus selected from the group consisting of PPGRP, GRGRGRGG, Appeal 2009-010657 Application 08/781,296

which describes the peptides defined by SEQ ID NOs: 1-3, 13, 14, 17-19, 21, 22, 25-33, 36, and 38 in claim 27 on appeal as reagents used to detect antibodies to peptides from Epstein-Barr virus (Spec. 62). This interpretation is also consistent with the explicit description in the Specification that

Peptides of up to about forty amino acids, more preferably between four and twenty-five amino acids, most preferably eight amino acids, can be synthesized using any one of the methods known to those skilled in the art. In general, an epitope of a protein is composed of between three or four and eight amino acids ... As used herein, the peptide can contain the entire native epitope, or portions thereof sufficient to react with autoantibody (Spec. at 20:26-36).

Having properly construed claim 27, we turn to the written description issue.

The test for determining compliance with the written description requirement is whether the disclosure of the application as originally filed reasonably conveys to the artisan that the inventor had possession at that time of the later claimed subject matter, rather than the presence or absence of literal support in the specification for the claim language. *In re Herschler*, 591 F.2d 693, 700 (CCPA 1979); *In re Edwards*, 568 F.2d 1349, 1351-52 (CCPA 1978). "[T]he PTO has the initial burden of presenting evidence of reasons why persons skilled in the art would not recognize in the disclosure a description of the invention defined by the claims." *In re Wertheim*, 541 F.2d 257, 263-64 (CCPA 1976).

Here, in our opinion, at least original claim 8 together with the disclosure at page 20, lines 26-36, of the Specification, as originally filed, reasonably convey to the artisan that Appellants had possession of the subject matter of claim 27. Both the structural and functional components of the claimed peptide composition are described, i.e., a peptide up to about forty amino acids containing an epitope reactive with autoantibody wherein the autoantibody-reactive epitope is a member of the Markush group of original claim 8.

To summarize, claim 27 recites a composition containing a peptide molecule with two required limitations – it consists of about forty amino acids or less and it contains a sequence selected from the recited Markush group. Since the Examiner's rejection is based on an improper interpretation of claim 27, we reverse the rejection of claims 27 and 29 under § 112, first paragraph, for lack of original descriptive support in view of the disclosure of the Specification at page 20 and in original claim 8.

III. Anticipation

The Examiner found that Figure 1A of Chen describes a peptide consisting of 40 amino acids or less and comprising peptide SEQ ID NOs:

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28, 29, and 30 (Ans. at 5). Thus, the Examiner found the subject matter of claim 27 anticipated by Chen (*id.*).

Appellants argue that Figure 1A does not disclose the sequence of a discrete peptide, but rather of an illustrated portion of a larger protein, EBNA-1 (App. Br. at 9-10). Thus, Appellants contend that Chen fails to satisfy the limitation of claim 27 of a peptide of about 40 amino acids or less (*id.* at 10). The Examiner replies that claim 27 is not limited to only a peptide composition "consisting of" 40 amino acids or less and, therefore, claim 27 is anticipated by Chen (Ans. at 10).

Based on the positions advanced by the Examiner and Appellants, the issue relative to the anticipation rejection is does Figure 1A of Chen describe a peptide composition within the scope of claim 27.

According to Chen, Figure 1A shows "[t]he location of the DNA recognition domain within the 641 aa [amino acid] EBNA-1 ... along with the amino acid sequence" (Chen at 489, legend of Figure 1).

A reference anticipates a claim under § 102(b) when it discloses each and every element of the claimed invention, either explicitly or inherently. In re Gleave, 560 F.3d 1331, 1334 (Fed. Cir. 2009).

Here, the peptide composition shown in Figure 1 of Chen is a 641 amino acid peptide, not a peptide of about 40 amino acids or less as required by claim 27. Therefore, we reverse the rejection of claims 27 and 29 under § 102 as anticipated by Chen. Figure 1A of Chen describe a peptide composition within the scope of claim 27.

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IV. Order

Upon consideration of the record, and for the reasons given, it is ORDERED that the decision of the Examiner to reject claims 27 and 29 under 35 U.S.C. § 112, first paragraph (lack of written descriptive support), is REVERSED, and

FURTHER ORDERED that the decision of the Examiner to reject claims 27 and 29 under 35 U.S.C. § 102(b) as anticipated by Chen is REVERSED.

REVERSED

alw

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